

SEQUENCE LISTING

<110> DARROW, ANDREW

QI, JENSON

ANDRADE-GORDON, PATRICIA

<120> ZYMOGEN ACTIVATION SYSTEM

<130> ORT-1028

<140>

<141>

<160> 60

<170> PATENTIN VER. 2.0

<210> 1

<211> 361

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

<400> 1

GAATTCACCA CCATGGACAG CAAAGGTTTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60
GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120
GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAT 180
GCTCTAGATA GCGGCCGCTT CCCTTTAGTG AGGGTTAATG CTTGAGCAG ACATGATAAG 240
ATACATTGAT GAGTTTGGAC AAACCACAAC TAGAATGCAG TGAAAAAAT GCTTTATTTG 300
TGAAATTTGT GATGCTATTG CTTTATTTGT AACCATTATA AGCTGCAATA AACAAGTTGA 360

C

361

<210> 2

<211> 301

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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TTTGATGATG ATGACAAGAT CGTTGGGGGC TATTGTCTAG ATACCCCTAC GATGTGCCCCG 120

ATTACGCCTA GCGGCCGCTT CCCTTTAGTG AGGGTTAATG CTTGAGCAG ACATGATAAG 180

ATACATTGAT GAGTTTGGAC AAACCACAAC TAGAATGCAG TGAAAAAAT GCTTTATTG 240

TGAAATTTGT GATGCTATTG CTTTATTGTT AACCATTATA AGCTGCAATA AACAAGTTGA 300

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301

<210> 3

<211> 484

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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GTGGTGTCAG ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120
GTGGACGCGG CCGCTCTTGC TGCCCCCTTT ATCGAGGGGC GCATTGTGGA GGGCTCGGAT 180
CTAGATACCC CTACGATGTG CCCGATTACG CCGCTAGATA CCCCTACGAT GTGCCCCGATT 240
ACGCCGCTAG ATACCACTAC GATGTGCCCCG ATTACGCCGC TAGATACCCC TACGATGTGC 300
CCGATTACGC CTAGCGGCCG CTTCCTTTTA GTGAGGGTTA ATGCTTCGAG CAGACATGAT 360
AAGATACATT GATGAGTTTG GACAAACCAC AACTAGAATG CAGTGAAAAA AATGCTTTAT 420
TTGTGAAATT TGTGATGCTA TTGCTTTATT TGTAACCATT ATAAGCTGCA ATAAACAAGT 480
TGAC 484

<210> 4

<211> 382

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAC 180

AACTGTCTAG ACATCACCAT CACCATCACT AGCGGCCGCT TCCCTTTAGT GAGGGTTAAT 240

GCTTCGAGCA GACATGATAA GATACATTGA TGAGTTTGGA CAAACCACAA CTAGAATGCA 300

GTGAAAAAAA TGCTTTATTT GTGAAATTTG TGATGCTATT GCTTTATTTG TAACCATTAT 360

AAGCTGCAAT AAACAAGTTG AC 382

<210> 5

<211> 352

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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GAATTCACCA CCATGGCTTT CCTCTGGCTC CTCTCCTGCT GGGCCCTCCT GGTACCACC 60
TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCCC 120
TTTGATGATG ATGACAAGAT CGTTGGGGGC TATGCTCTAG ACATCACCAT CACCATCACT 180
AGCGGCCGCT TCCCTTTAGT GAGGGTTAAT GCTTCGAGCA GACATGATAA GATACATTGA 240
TGAGTTTGGA CAAACCACAA CTAGAATGCA GTGAAAAAAA TGCTTTATTT GTGAAATTTG 300
TGATGCTATT GCTTTATTTG TAACCATTAT AAGCTGCAAT AAACAAGTTG AC 352

<210> 6

<211> 385

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCCC 120
TTTGATGATG ATGACAAGAT CGTTGGGGGC TATGCTCTAG ATACCCCTAC GATGTGCCCC 180
ATTACGCCGC TAGACATCAC CATCACCATC ACTAGCGGCC GCTTCCCTTT AGTGAGGGTT 240
AATGCTTCGA GCAGACATGA TAAGATACAT TGATGAGTTT GGACAAACCA CAACTAGAAT 300
GCAGTGAAAA AAATGCTTTA TTTGTGAAAT TTGTGATGCT ATTGCTTTAT TTGTAACCAT 360
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<210> 7

<211> 1169

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 7

GAATTCACCA CCATGGACAG CAAAGGTTTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60
GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120
GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAT 180
GCTCTAGAGG CCGGTCAGTG GCCCTGGCAG GTCAGCATCA CCTATGAAGG CGTCCATGTG 240
TGTGGTGGCT CTCTCGTGTC TGAGCAGTGG GTGCTGTCAG CTGCTCACTG CTTCCCCAGC 300
GAGCACCACA AGGAAGCCTA TGAGGTCAAG CTGGGGGCCC ACCAGCTAGA CTCCTACTCC 360
GAGGACGCCA AGGTCAGCAC CCTGAAGGAC ATCATCCCCC ACCCCAGCTA CCTCCAGGAG 420
GGCTCCCAGG GCGACATTGC ACTCCTCCAA CTCAGCAGAC CCATCACCTT CTCCCCTAC 480
ATCCGGCCCA TCTGCCTCCC TGCAGCCAAC GCCTCCTTCC CCAACGGCCT CCACTGCACT 540

GTCACTGGCT GGGGTCATGT GGCCCCCTCA GTGAGCCTCC TGACGCCCAA GCCACTGCAG 600
CAACTCGAGG TGCCTCTGAT CAGTCGTGAG ACGTGTAAC TGCCTGTACAA CATCGACGCC 660
AAGCCTGAGG AGCCGCACTT TGTCCAAGAG GACATGGTGT GTGCTGGCTA TGTGGAGGGG 720
GGCAAGGACG CCTGCCAGGG TGACTCTGGG GGCCCCACTCT CCTGCCCTGT GGAGGGTCTC 780
TGGTACCTGA CGGGCATTTGT GAGCTGGGGA GATGCCTGTG GGGCCCGCAA CAGGCCTGGT 840
GTGTACACTC TGGCCTCCAG CTATGCCTCC TGGATCCAAA GCAAGGTGAC AGAACTCCAG 900
CCTCGTGTGG TGCCCCAAAC CCAGGAGTCC CAGCCCGACA GCAACCTCTG TGGCAGCCAC 960
CTGGCCTTCA GCTCTAGACA TCACCATCAC CATCACTAGC GGCCGCTTCC CTTTAGTGAG 1020
GGTTAATGCT TCGAGCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAATA 1080
GAATGCAGTG AAAAAAATGC TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA 1140
CCATTATAAG CTGCAATAAA CAAGTTGAC 1169

<210> 8

<211> 1142

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 8

GAATTCACCA CCATGGCTTT CCTCTGGCTC CTCTCCTGCT GGGCCCTCCT GGGTACCACC 60
TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCCC 120
TTTGATGATG ATGACAAGAT CGTTGGGGGC TATGCTCTAG AGGCCGGTCA GTGGCCCTGG 180
CAGGTCAGCA TCACCTATGA AGGCGTCCAT GTGTGTGGTG GCTCTCTCGT GTCTGAGCAG 240
TGGGTGCTGT CAGCTGCTCA CTGCTTCCCC AGCGAGCACC ACAAGGAAGC CTATGAGGTC 300
AAGCTGGGGG CCCACCAGCT AGACTCCTAC TCCGAGGACG CCAAGGTCAG CACCCTGAAG 360
GACATCATCC CCCACCCAG CTACCTCCAG GAGGGCTCCC AGGGCGACAT TGCACTCCTC 420
CAACTCAGCA GACCCATCAC CTTCTCCCGC TACATCCGGC CCATCTGCCT CCCTGCAGCC 480
AAGCCTCCT TCCCCAACGG CCTCCACTGC ACTGTCACTG GCTGGGGTCA TGTGGCCCCC 540
TCAGTGAGCC TCCTGACGCC CAAGCCACTG CAGCAACTCG AGGTGCCTCT GATCAGTCGT 600
GAGACGTGTA ACTGCCTGTA CAACATCGAC GCCAAGCCTG AGGAGCCGCA CTTTGTCCAA 660
GAGGACATGG TGTGTGCTGG CTATGTGGAG GGGGGCAAGG ACGCCTGCCA GGGTGA CTCT 720
GGGGGCCCC TCTCCTGCCC TGTGGAGGGT CTCTGGTACC TGACGGGCAT TGTGAGCTGG 780
GGAGATGCCT GTGGGGCCCG CAACAGGCCT GGTGTGTACA CTCTGGCCTC CAGCTATGCC 840

TCCTGGATCC AAAGCAAGGT GACAGAACTC CAGCCTCGTG TGGTGCCCCA AACCCAGGAG 900
TCCCAGCCCCG ACAGCAACCT CTGTGGCAGC CACCTGGCCT TCAGCTCTAG ACATCACCAT 960
CACCATCACT AGCGGCCGCT TCCCTTTAGT GAGGGTTAAT GCTTCGAGCA GACATGATAA 1020
GATACATTGA TGAGTTTGGA CAAACCACAA CTAGAATGCA GTGAAAAAAA TGCTTTATTT 1080
GTGAAATTTG TGATGCTATT GCTTTATTTG TAACCATTAT AAGCTGCAAT AAACAAGTTG 1140
AC 1142

<210> 9

<211> 1049

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

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GTGGTGTCAG ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120
 GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAC 180
 AACTGTCTAG AACCCCATTC GCAGCCTTGG CAGGCGGCCT TGTTCAGGG CCAGCAACTA 240
 CTCTGTGGCG GTGTCCTTGT AGGTGGCAAC TGGGTCCTTA CAGCTGCCCA CTGTAAAAAA 300
 CCGAAATACA CAGTACGCCT GGGAGACCAC AGCCTACAGA ATAAAGATGG CCCAGAGCAA 360
 GAAATACCTG TGGTTCAGTC CATCCACAC CCCTGCTACA ACAGCAGCGA TGTGGAGGAC 420
 CACAACCATG ATCTGATGCT TCTTCAACTG CGTGACCAGG CATCCCTGGG GTCCAAAGTG 480
 AAGCCCATCA GCCTGGCAGA TCATTGCACC CAGCCTGGCC AGAAGTGCAC CGTCTCAGGC 540
 TGGGGCACTG TCACCAGTCC CCGAGAGAAT TTTCTGACA CTCTCAACTG TGCAGAAGTA 600
 AAAATCTTTC CCCAGAAGAA GTGTGAGGAT GCTTACCCGG GGCAGATCAC AGATGGCATG 660
 GTCTGTGCAG GCAGCAGCAA AGGGGCTGAC ACGTGCCAGG GCGATTCTGG AGGCCCCCTG 720
 GTGTGTGATG GTGCACTCCA GGGCATCACA TCCTGGGGCT CAGACCCCTG TGGGAGGTCC 780
 GACAAACCTG GCGTCTATAC CAACATCTGC CGCTACCTGG ACTGGATCAA GAAGATCATA 840
 GGCAGCAAGG GCTCTAGACA TCACCATCAC CATCACTAGC GGCCGCTTCC CTTTAGTGAG 900
 GGTTAATGCT TCGAGCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAATA 960
 GAATGCAGTG AAAAAAATGC TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA 1020
 CCATTATAAG CTGCAATAAA CAAGTTGAC 1049

<210> 10

<211> 1052

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 10

GAATTCACCA CCATGGACAG CAAAGGTTTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60
GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120
GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAC 180
AACTGTCTAG AAAAGCACTC CCAGCCCTGG CAGGCAGCCC TGTTCGAGAA GACGCGGCTA 240
CTCTGTGGGG CGACGCTCAT CGCCCCAGA TGGCTCCTGA CAGCAGCCCA CTGCCTCAAG 300
CCCCGCTACA TAGTTCACCT GGGGCAGCAC AACCTCCAGA AGGAGGAGGG CTGTGAGCAG 360
ACCCGGACAG CCACTGAGTC CTTCCCCAC CCCGGCTTCA ACAACAGCCT CCCCAACAAA 420
GACCACCGCA ATGACATCAT GCTGGTGAAG ATGGCATCGC CAGTCTCCAT CACCTGGGCT 480

GTGCGACCCC TCACCCTCTC CTCACGCTGT GTCACTGCTG GCACCAGCTG CCTCATTTCC 540
GGCTGGGGCA GCACGTCCAG CCCCAGTTA CGCCTGCCTC ACACCTTGCG ATGCGCCAAC 600
ATCACCATCA TTGAGCACCA GAAGTGTGAG AACGCCTACC CCGGCAACAT CACAGACACC 660
ATGGTGTGTG CCAGCGTGCA GGAAGGGGGC AAGGACTCCT GCCAGGGTGA CTCCGGGGGC 720
CCTCTGGTCT GTAACCAGTC TCTTCAAGGC ATTATCTCCT GGGGCCAGGA TCCGTGTGCG 780
ATCACCCGAA AGCCTGGTGT CTACACGAAA GTCTGCAAAT ATGTGGACTG GATCCAGGAG 840
ACGATGAAGA ACAATTCTAG ACATCACCAT CACCATCACT AGCGGCCGCT TCCCTTTAGT 900
GAGGGTTAAT GCTTCGAGCA GACATGATAA GATACATTGA TGAGTTTGGA CAAACCACAA 960
CTAGAATGCA GTGAAAAAAA TGCTTTATTT GTGAAATTTG TGATGCTATT GCTTTATTTG 1020
TAACCATTAT AAGCTGCAAT AAACAAGTTG AC 1052

<210> 11

<211> 328

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 11

MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU LEU

1

5

10

15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20

25

30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35

40

45

ASP ASP LYS ILE VAL GLY GLY TYR ALA LEU GLU ALA GLY GLN TRP PRO

50

55

60

TRP GLN VAL SER ILE THR TYR GLU GLY VAL HIS VAL CYS GLY GLY SER

65

70

75

80

LEU VAL SER GLU GLN TRP VAL LEU SER ALA ALA HIS CYS PHE PRO SER

85

90

95

GLU HIS HIS LYS GLU ALA TYR GLU VAL LYS LEU GLY ALA HIS GLN LEU

100

105

110

ASP SER TYR SER GLU ASP ALA LYS VAL SER THR LEU LYS ASP ILE ILE

115

120

125

PRO HIS PRO SER TYR LEU GLN GLU GLY SER GLN GLY ASP ILE ALA LEU

130

135

140

LEU GLN LEU SER ARG PRO ILE THR PHE SER ARG TYR ILE ARG PRO ILE

145

150

155

160

CYS LEU PRO ALA ALA ASN ALA SER PHE PRO ASN GLY LEU HIS CYS THR

165

170

175

VAL THR GLY TRP GLY HIS VAL ALA PRO SER VAL SER LEU LEU THR PRO

180

185

190

LYS PRO LEU GLN GLN LEU GLU VAL PRO LEU ILE SER ARG GLU THR CYS

195

200

205

ASN CYS LEU TYR ASN ILE ASP ALA LYS PRO GLU GLU PRO HIS PHE VAL

210

215

220

GLN GLU ASP MET VAL CYS ALA GLY TYR VAL GLU GLY GLY LYS ASP ALA

225

230

235

240

CYS GLN GLY ASP SER GLY GLY PRO LEU SER CYS PRO VAL GLU GLY LEU

245

250

255

TRP TYR LEU THR GLY ILE VAL SER TRP GLY ASP ALA CYS GLY ALA ARG

260

265

270

ASN ARG PRO GLY VAL TYR THR LEU ALA SER SER TYR ALA SER TRP ILE

275

280

285

GLN SER LYS VAL THR GLU LEU GLN PRO ARG VAL VAL PRO GLN THR GLN

290

295

300

GLU SER GLN PRO ASP SER ASN LEU CYS GLY SER HIS LEU ALA PHE SER

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315

320

SER ARG HIS HIS HIS HIS HIS HIS

325

<210> 12

<211> 319

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 12

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1

5

10

15

PHE GLY CYS GLY VAL PRO ASP TYR LYS ASP ASP ASP ASP ALA ALA ALA

20

25

30

LEU ALA ALA PRO PHE ASP ASP ASP ASP LYS ILE VAL GLY GLY TYR ALA

35

40

45

LEU GLU ALA GLY GLN TRP PRO TRP GLN VAL SER ILE THR TYR GLU GLY

50

55

60

VAL HIS VAL CYS GLY GLY SER LEU VAL SER GLU GLN TRP VAL LEU SER

83

65

70

75

80

ALA ALA HIS CYS PHE PRO SER GLU HIS HIS LYS GLU ALA TYR GLU VAL

85

90

95

LYS LEU GLY ALA HIS GLN LEU ASP SER TYR SER GLU ASP ALA LYS VAL

100

105

110

SER THR LEU LYS ASP ILE ILE PRO HIS PRO SER TYR LEU GLN GLU GLY

115

120

125

SER GLN GLY ASP ILE ALA LEU LEU GLN LEU SER ARG PRO ILE THR PHE

130

135

140

SER ARG TYR ILE ARG PRO ILE CYS LEU PRO ALA ALA ASN ALA SER PHE

145

150

155

160

PRO ASN GLY LEU HIS CYS THR VAL THR GLY TRP GLY HIS VAL ALA PRO

84

165

170

175

SER VAL SER LEU LEU THR PRO LYS PRO LEU GLN GLN LEU GLU VAL PRO

180

185

190

LEU ILE SER ARG GLU THR CYS ASN CYS LEU TYR ASN ILE ASP ALA LYS

195

200

205

PRO GLU GLU PRO HIS PHE VAL GLN GLU ASP MET VAL CYS ALA GLY TYR

210

215

220

VAL GLU GLY GLY LYS ASP ALA CYS GLN GLY ASP SER GLY GLY PRO LEU

225

230

235

240

SER CYS PRO VAL GLU GLY LEU TRP TYR LEU THR GLY ILE VAL SER TRP

245

250

255

GLY ASP ALA CYS GLY ALA ARG ASN ARG PRO GLY VAL TYR THR LEU ALA

85

260

265

270

SER SER TYR ALA SER TRP ILE GLN SER LYS VAL THR GLU LEU GLN PRO

275

280

285

ARG VAL VAL PRO GLN THR GLN GLU SER GLN PRO ASP SER ASN LEU CYS

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GLY SER HIS LEU ALA PHE SER SER ARG HIS HIS HIS HIS HIS HIS

305

310

315

<210> 13

<211> 288

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 13

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1 5 10 15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20 25 30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35 40 45

ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU PRO HIS SER GLN

50 55 60

PRO TRP GLN ALA ALA LEU PHE GLN GLY GLN GLN LEU LEU CYS GLY GLY

65 70 75 80

VAL LEU VAL GLY GLY ASN TRP VAL LEU THR ALA ALA HIS CYS LYS LYS

85

90

95

PRO LYS TYR THR VAL ARG LEU GLY ASP HIS SER LEU GLN ASN LYS ASP

100

105

110

GLY PRO GLU GLN GLU ILE PRO VAL VAL GLN SER ILE PRO HIS PRO CYS

115

120

125

TYR ASN SER SER ASP VAL GLU ASP HIS ASN HIS ASP LEU MET LEU LEU

130

135

140

GLN LEU ARG ASP GLN ALA SER LEU GLY SER LYS VAL LYS PRO ILE SER

145

150

155

160

LEU ALA ASP HIS CYS THR GLN PRO GLY GLN LYS CYS THR VAL SER GLY

165

170

175

TRP GLY THR VAL THR SER PRO ARG GLU ASN PHE PRO ASP THR LEU ASN

180

185

190

CYS ALA GLU VAL LYS ILE PHE PRO GLN LYS LYS CYS GLU ASP ALA TYR

195

200

205

PRO GLY GLN ILE THR ASP GLY MET VAL CYS ALA GLY SER SER LYS GLY

210

215

220

ALA ASP THR CYS GLN GLY ASP SER GLY GLY PRO LEU VAL CYS ASP GLY

225

230

235

240

ALA LEU GLN GLY ILE THR SER TRP GLY SER ASP PRO CYS GLY ARG SER

245

250

255

ASP LYS PRO GLY VAL TYR THR ASN ILE CYS ARG TYR LEU ASP TRP ILE

260

265

270

LYS LYS ILE ILE GLY SER LYS GLY SER ARG HIS HIS HIS HIS HIS HIS

275

280

285

<210> 14

<211> 289

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 14

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1 5 10 15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20 25 30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35 40 45

ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU LYS HIS SER GLN

50 55 60

PRO TRP GLN ALA ALA LEU PHE GLU LYS THR ARG LEU LEU CYS GLY ALA

65 70 75 80

THR LEU ILE ALA PRO ARG TRP LEU LEU THR ALA ALA HIS CYS LEU LYS

85 90 95

PRO ARG TYR ILE VAL HIS LEU GLY GLN HIS ASN LEU GLN LYS GLU GLU

100

105

110

GLY CYS GLU GLN THR ARG THR ALA THR GLU SER PHE PRO HIS PRO GLY

115

120

125

PHE ASN ASN SER LEU PRO ASN LYS ASP HIS ARG ASN ASP ILE MET LEU

130

135

140

VAL LYS MET ALA SER PRO VAL SER ILE THR TRP ALA VAL ARG PRO LEU

145

150

155

160

THR LEU SER SER ARG CYS VAL THR ALA GLY THR SER CYS LEU ILE SER

165

170

175

GLY TRP GLY SER THR SER SER PRO GLN LEU ARG LEU PRO HIS THR LEU

180

185

190

ARG CYS ALA ASN ILE THR ILE ILE GLU HIS GLN LYS CYS GLU ASN ALA

195

200

205

TYR PRO GLY ASN ILE THR ASP THR MET VAL CYS ALA SER VAL GLN GLU

210

215

220

GLY GLY LYS ASP SER CYS GLN GLY ASP SER GLY GLY PRO LEU VAL CYS

225

230

235

240

ASN GLN SER LEU GLN GLY ILE ILE SER TRP GLY GLN ASP PRO CYS ALA

245

250

255

ILE THR ARG LYS PRO GLY VAL TYR THR LYS VAL CYS LYS TYR VAL ASP

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265

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TRP ILE GLN GLU THR MET LYS ASN ASN SER ARG HIS HIS HIS HIS HIS

275

280

285

HIS

<210> 15

<211> 9

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 15

CTAGATAGC

9

<210> 16

<211> 9

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 16

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9

<210> 17

<211> 36

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

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36

<210> 18

<211> 36

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 18

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<210> 19

<211> 33

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 19

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<210> 20

<211> 33

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 20

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<210> 21

<211> 27

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 21

CTAGACATCA CCATCACCAT CACTAGC

27

<210> 22

<211> 27

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 22

GGCCGCTAGT GATGGTGATG GTGATGT

27

<210> 23

<211> 34

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 23

TGAATTCACC ACCATGGACA GCAAAGGTTG GTCG

34

<210> 24

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 24

CAGAAAGGGT CCCGCCTGCT CCTGCTGCTG

30

<210> 25

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 25

GTGGTGTCAA ATCTACTCTT TGCCAGGGT

30

<210> 26

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

Sequence

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 28

TAATAATGCG GCCGCGTCCA CGTCGTCGTC GTCCT

35

<210> 29

<211> 21

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 29

TGTAGTCGGA GACCACACCC T

21

<210> 30

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 30

GGCACAAGAG TAGATTGAC ACCACCAGCA

30

<210> 31

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 31

GCAGGAGCAG GCGGGACCCT TTCTGCGACG

30

<210> 32

<211> 29

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 32

AACCTTTGCT GTCCATGGTG GTGAATTCA

29

<210> 33

<211> 40

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 33

AATTCACCAT GAATCCACTC CTGATCCTTA CCTTTGTGGC

40

<210> 34

<211> 40

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 34

GGCCGCCACA AAGGTAAGGA TCAGGAGTGG ATTCATGGTG

40

<210> 35

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 35

AATTCACCAC CATGGCTTTC CTCTGGCTCC TCTCCTGCTG GGCCCTCCTG GGTAC 55

<210> 36

<211> 47

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 36

CCAGGAGGGC CCAGCAGGAG AGGAGCCAGA GGAAAGCCAT GGTGGTG 47

<210> 37

<211> 45

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 37

CACCTTCGGC TCGGGGTCC CCGACTACAA GGACGACGAC GACGC

45

<210> 38

<211> 53

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 38

GGCCGCGTCG TCGTCGTCCT TGTCGTCGGG GACCCCGCAG CCGAAGGTGG TAC

53

<210> 39

<211> 29

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 39

GTGGCGGCCG CTCTTGCTGC CCCCTTTGA

29

<210> 40

<211> 28

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 40

TTCTCTAGAC AGTTGTAGCC CCCAACGA

28

<210> 41

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 41

GGCCGCTCTT GCTGCCCCCT TTGATGATGA TGACAAGATC GTTGGGGGCT ATGCT 55

<210> 42

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 42

CTAGAGCATA GCCCCAACG ATCTTGTCAT CATCATCAAA GGGGGCAGCA AGAGC 55

<210> 43

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 43

GGCCGCTCTT GCTGCCCCCT TTGATGATGA TGACAAGATC GTTGGGGGCT ATTGT 55

<210> 44

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 44

CTAGACAATA GCCCCCAACG ATCTTGTCAT CATCATCAAA GGGGGCAGCA AGAGC 55

<210> 45

<211> 52

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 45

GGCCGCTCTT GCTGCCCCCT TTATCGAGGG GCGCATTGTG GAGGGCTCGG AT 52

<210> 46

<211> 52

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 46

CTAGATCCGA GCCCTCCACA ATGCGCCCCT CGATAAAGGG GGCAGCAAGA GC

52

<210> 47

<211> 32

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 47

AGCAGTCTAG AGGCCGGTCA GTGGCCCTGG CA

32

<210> 48

<211> 28

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 48

GCTGGTCTAG AGCTGAAGGC CAGGTGGC

28

<210> 49

<211> 29

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 49

GGTATCTAGA GCCCTTGCTG CCTATGATC

29

<210> 50

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 50

ACTGTCTAGA ACCCCATTCG CAGCCTTGGC

30

<210> 51

<211> 32

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 51

TCGATCTAGA AAAGCACTCC CAGCCCTGGC AG

32

<210> 52

<211> 32

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 52

GTCCTCTAGA ATTGTTCTTC ATCGTCTCCT GG

32

<210> 53

<211> 306

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE OF

HUMAN PROTEASE F IN CFEK2 ZYMOGEN VECTOR

<400> 53

MET ALA PHE LEU TRP LEU LEU SER CYS TRP ALA LEU LEU GLY THR THR

1 5 10 15

PHE GLY CYS GLY VAL PRO ASP TYR LYS ASP ASP ASP ASP ALA ALA ALA

20 25 30

LEU ALA ALA PRO PHE ASP ASP ASP ASP LYS ILE VAL GLY GLY TYR ALA

35 40 45

LEU GLU LEU GLY ARG TRP PRO TRP GLN GLY SER LEU ARG LEU TRP ASP

50 55 60

SER HIS VAL CYS GLY VAL SER LEU LEU SER HIS ARG TRP ALA LEU THR

65 70 75 80

ALA ALA HIS CYS PHE GLU THR TYR SER ASP LEU SER ASP PRO SER GLY

120

85

90

95

TRP MET VAL GLN PHE GLY GLN LEU THR SER MET PRO SER PHE TRP SER

100

105

110

LEU GLN ALA TYR TYR ASN ARG TYR PHE VAL SER ASN ILE TYR LEU SER

115

120

125

PRO ARG TYR LEU GLY ASN SER PRO TYR ASP ILE ALA LEU VAL LYS LEU

130

135

140

SER ALA PRO VAL THR TYR THR LYS HIS ILE GLN PRO ILE CYS LEU GLN

145

150

155

160

ALA SER THR PHE GLU PHE GLU ASN ARG THR ASP CYS TRP VAL THR GLY

165

170

175

TRP GLY TYR ILE LYS GLU ASP GLU ALA LEU PRO SER PRO HIS THR LEU

121

180

185

190

GLN GLU VAL GLN VAL ALA ILE ILE ASN ASN SER MET CYS ASN HIS LEU

195

200

205

PHE LEU LYS TYR SER PHE ARG LYS ASP ILE PHE GLY ASP MET VAL CYS

210

215

220

ALA GLY ASN ALA GLN GLY GLY LYS ASP ALA CYS PHE GLY ASP SER GLY

225

230

235

240

GLY PRO LEU ALA CYS ASN LYS ASN GLY LEU TRP TYR GLN ILE GLY VAL

245

250

255

VAL SER TRP GLY VAL GLY CYS GLY ARG PRO ASN ARG PRO GLY VAL TYR

260

265

270

THR ASN ILE SER HIS HIS PHE GLU TRP ILE GLN LYS LEU MET ALA GLN

122

275

280

285

SER GLY MET SER GLN PRO ASP PRO SER TRP SER ARG HIS HIS HIS HIS

290

295

300

HIS HIS

305

<210> 54

<211> 284

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: HUMAN MH2

PROTEASE IN PFEK ZYMOGEN VECTOR

<400> 54

MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU LEU

1 5 10 15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20 25 30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35 40 45

ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU PRO HIS SER GLN

50 55 60

PRO TRP GLN ALA ALA LEU VAL MET GLU ASN GLU LEU PHE CYS SER GLY

65 70 75 80

VAL LEU VAL HIS PRO GLN TRP VAL LEU SER ALA ALA HIS CYS PHE GLN

85 90 95

ASN SER TYR THR ILE GLY LEU GLY LEU HIS SER LEU GLU ALA ASP GLN

100

105

110

GLU PRO GLY SER GLN MET VAL GLU ALA SER LEU SER VAL ARG HIS PRO

115

120

125

GLU TYR ASN ARG PRO LEU LEU ALA ASN ASP LEU MET LEU ILE LYS LEU

130

135

140

ASP GLU SER VAL SER GLU SER ASP THR ILE ARG SER ILE SER ILE ALA

145

150

155

160

SER GLN CYS PRO THR ALA GLY ASN SER CYS LEU VAL SER GLY TRP GLY

165

170

175

LEU LEU ALA ASN GLY ARG MET PRO THR VAL LEU GLN CYS VAL ASN VAL

180

185

190

SER VAL VAL SER GLU GLU VAL CYS SER LYS LEU TYR ASP PRO LEU TYR

195

200

205

HIS PRO SER MET PHE CYS ALA GLY GLY GLY HIS ASP GLN LYS ASP SER

210

215

220

CYS ASN GLY ASP SER GLY GLY PRO LEU ILE CYS ASN GLY TYR LEU GLN

225

230

235

240

GLY LEU VAL SER PHE GLY LYS ALA PRO CYS GLY GLN VAL GLY VAL PRO

245

250

255

GLY VAL TYR THR ASN LEU CYS LYS PHE THR GLU TRP ILE GLU LYS THR

260

265

270

VAL GLN ALA SER SER ARG HIS HIS HIS HIS HIS HIS

275

280

<210> 55

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

<400> 55

AGGATCTAGA GCCGCACTCG CAGCCCTGGC

30

<210> 56

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

<400> 56

CCCATCTAGA ACTGGCCTGG ACGGTTTTCT

30

<210> 57

<211> 32

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

<400> 57

AGGATCTAGA ACTCGGGCGT TGGCCGTGGC AG

32

<210> 58

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

<400> 58

AGAGTCTAGA CCAGGAGGGG TCTGGCTGGG

30

<210> 59

<211> 1103

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: NUCLEIC ACID

SEQUENCE OF HUMAN PROTEASE F IN CFEK2 ZYMOGEN

VECTOR

<400> 59

GAATTCACCA CCATGGCTTT CCTCTGGCTC CTCTCCTGCT GGGCCCTCCT GGGTACCACC 60
TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCCC 120
TTTGATGATG ATGACAAGAT CGTTGGGGGC TATGCTCTAG AACTCGGGCG TTGGCCGTGG 180
CAGGGGAGCC TGC GCCTGTG GGATTCCCAC GTATGCGGAG TGAGCCTGCT CAGCCACCGC 240
TGGGCACTCA CGGCGGCGCA CTGCTTTGAA ACCTATAGTG ACCTTAGTGA TCCCTCCGGG 300
TGGATGGTCC AGTTTGGCCA GCTGACTTCC ATGCCATCCT TCTGGAGCCT GCAGGCCTAC 360
TACAACCGTT ACTTCGTATC GAATATCTAT CTGAGCCCTC GCTACCTGGG GAATTCACCC 420
TATGACATTG CCTTGGTGAA GCTGTCTGCA CCTGTCACCT AACTAAACA CATCCAGCCC 480
ATCTGTCTCC AGGCCTCCAC ATTTGAGTTT GAGAACCGGA CAGACTGCTG GGTGACTGGC 540
TGGGGGTACA TCAAAGAGGA TGAGGCACTG CCATCTCCCC ACACCCTCCA GGAAGTTCAG 600
GTCGCCATCA TAAACAACTC TATGTGCAAC CACCTCTTCC TCAAGTACAG TTTCCGCAAG 660
GACATCTTTG GAGACATGGT TTGTGCTGGC AATGCCCAAG GCGGGAAGGA TGCCTGCTTC 720
GGTGA CTCAG GTGGACCCTT GGCCTGTAAC AAGAATGGAC TGTGGTATCA GATTGGAGTC 780
GTGAGCTGGG GAGTGGGCTG TGGTCGGCCC AATCGGCCCG GTGTCTACAC CAATATCAGC 840
CACCAC TTTG AGTGGATCCA GAAGCTGATG GCCCAGAGTG GCATGTCCCA GCCAGACCCC 900

TCCTGGTCTA GACATCACCA TCACCATCAC TAGCGGCCGC TTCCCTTTAG TGAGGGTTAA 960
TGCTTCGAGC AGACATGATA AGATACATTG ATGAGTTTGG ACAAACCACA ACTAGAATGC 1020
AGTGAAAAAA ATGCTTTATT TGTGAAATTT GTGATGCTAT TGCTTTATTT GTAACCATTA 1080
TAAGCTGCAA TAAACAAGTT GAC 1103

<210> 60

<211> 1037

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: NUCLEIC ACID

SEQUENCE OF HUMAN MH2 PROTEASE IN PFEK ZYMOGEN

VECTOR

<400> 60

GAATTCACCA CCATGGACAG CAAAGGTTTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60
GTGGTGTCAG ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAC 180
 AACTGTCTAG AGCCGCACTC GCAGCCCTGG CAGGCGGCAC TGGTCATGGA AAACGAATTG 240
 TTCTGCTCGG GCGTCCTGGT GCATCCGCAG TGGGTGCTGT CAGCCGCACA CTGTTTCCAG 300
 AACTCCTACA CCATCGGGCT GGGCCTGCAC AGTCTTGAGG CCGACCAAGA GCCAGGGAGC 360
 CAGATGGTGG AGGCCAGCCT CTCCGTACGG CACCCAGAGT ACAACAGACC CTTGCTCGCT 420
 AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG AGTCTGACAC CATCCGGAGC 480
 ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACCTTT GCCTCGTTTC TGGCTGGGGT 540
 CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG TGAACGTGTC GGTGGTGTCT 600
 GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGTACCACC CCAGCATGTT CTGCGCCGGC 660
 GGAGGGCACG ACCAGAAGGA CTCCTGCAAC GGTGACTCTG GGGGGCCCCT GATCTGCAAC 720
 GGGTACTTGC AGGGCCTTGT GTCTTTCGGA AAAGCCCCGT GTGGCCAAGT TGGCGTGCCA 780
 GGTGTCTACA CCAACCTCTG CAAATTCAC T GAGTGGATAG AGAAAACCGT CCAGGCCAGT 840
 TCTAGACATC ACCATCACCA TCACTAGCGG CCGCTTCCCT TTAGTGAGGG TTAATGCTTC 900
 GAGCAGACAT GATAAGATAC ATTGATGAGT TTGGACAAAC CACAACTAGA ATGCAGTGAA 960
 AAAAATGCTT TATTTGTGAA ATTTGTGATG CTATTGCTTT ATTTGTAACC ATTATAAGCT 1020
 GCAATAAACA AGTTGAC 1037